Amendments to the Specification:

Please amend the paragraph beginning on page 18, line 12, as follows:

--Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci.* USA 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.--

Please amend the paragraph beginning on page 52, line 20, as follows:

-- Subtracted cDNAs were cloned into pBluescript-based plasmid vectors to generate a subtracted cDNA library. 930 clones from the subtracted library were then chosen for sequence analysis. DNA sequences were mined using Blast searches against nucleotide and protein databases provided at, *e.g.*, the National Center for Biotechnology Information web site ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~. All sequences were also analyzed for the presence of potential transmembrane segments ~~(http://dot.imgen.bcm.tmc.edu:9331/seq-search/struc-~~

~~predict.html)~~. cDNAs encoding novel sequences were used in *in situ* hybridizations to tongue tissue sections to examine taste cell expression.--

Please amend the paragraph beginning on page 53, line 27, as follows:

-- TC-ICS encoding nucleic acids (e.g., SEQ ID NO:1, SEQ ID NO:4 or SEQ ID NO:7) are expressed in a heterologous cell, alone or with other cell transduction proteins such as a G-protein α subunit and/ or a taste cell specific G-protein coupled receptor such as GPCR-B3, GPCR-B4 (*see* U.S.S.N. 60/094,465 filed July 28, 1998 for the description of GPCR-B3 and U.S.S.N. 60/095,464 filed July 28, 1998 and 60/112,747 filed December 17, 1998 for the description of GPCR-B4), Gα14 or Gα15 (Wilkie *et al., PNAS USA* 88:10049-10053 (1991)). These transformed cells are used to screen for activators, inhibitors, and modulators of TC-ICS, including ~~mdulatorts~~ modulators of its ~~intewraction~~ interaction with GPCRs or G-proteins. Different assays for ion channel mediated functions are performed as generally described above and in PCT 99/06307, incorporated by reference herein.--